



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SUN, Yi
- (ii) TITLE OF INVENTION: SAG: Sensitive to Apoptosis Gene
- (iii) NUMBER OF SEQUENCES: 50
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Warner-Lambert Company
 - (B) STREET: 2800 Plymouth Road
 - (C) CITY: Ann Arbor
 - (D) STATE: Michigan
 - (E) COUNTRY: USA
 - (F) ZIP: 48105
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/509,779
 - (B) FILING DATE: 03-29-2000
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: David R. Kurlandsky
 - (B) REGISTRATION NUMBER: 41,505
 - (C) REFERENCE/DOCKET NUMBER: 5650-01-DRK
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 734-622-7304
 - (B) TELEFAX: 734-622-1553

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1140 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:17..355
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION:17..355

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..1140
- (D) OTHER INFORMATION:/note= "Mouse SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTTCTGCGCC GCCGCC ATG GCC GAC GTG GAG GAC GGC GAG GAA CCC TGC 49
 Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys
 1 5 10

GTC CTT TCT TCG CAC TCC GGG AGC GCA GGC TCC AAG TCG GGA GGC GAC 97
 Val Leu Ser Ser His Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp
 15 20 25

AAG ATG TTC TCT CTC AAG AAG TGG AAC GCG GTC GCA ATG TGG AGC TGG 145
 Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp
 30 35 40

GAC GTT GAG TGC GAT ACC TGT GCC ATC TGC AGG GTC CAG GTG ATG GAT 193
 Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp
 45 50 55

GCC TGC CTT CGA TGT CAA GCT GAA AAC AAG CAA GAG GAC TGT GTT GTG 241
 Ala Cys Leu Arg Cys Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val
 60 65 70 75

GTC TGG GGA GAG TGT AAC CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG 289
 Val Trp Gly Glu Cys Asn His Ser Phe His Asn Cys Cys Met Ser Leu
 80 85 90

TGG GTG AAA CAG AAC AAT CGC TGC CCT CTG TGC CAG CAG GAC TGG GTA 337
 Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val
 95 100 105

GTC CAA AGA ATC GGC AAA TGAGAGGTGG CCCAGGCGCT CCTGGTGTGG 385
 Val Gln Arg Ile Gly Lys
 110

TTGCTGACCC TGGACAAAGA CTAAACACTG CAGGGGATTC ATCCTTGAGA GAGAGAGGAT 445
 GCTGTGCGCC TTTGAGACTC ACCAAAGGCT TGCTTATTA ATTTGTCTGT TTAGTTTGG 505
 GAAATTCTCT ACAATTAAAGA TAATTTGTTA AAAATGGCCT TTCCTACCTC TGGTGTGTGT 565
 GTGTGATACG AATGCATAGA AGAGCGAGAA CACCAGAAAA TGATCTTGT TTATCTGTAC 625
 CCACGACTGG AACATTGTGT TCACAGAAGA ACATTGTTG TGTTTATGCT TGAGGGTTAA 685
 AAAATAGATA AACGAATGTT ACAGTAACAA ATAAAATGCA TTGAAAAGCC GACTCCTCCT 745
 AATCCTTTT GTGTTGGGAG AGAGGCAAGC GAGGCCACCC TGCTGTCTTC ATTTGCTGTG 805
 AATGAGGATT TTAACCTGCA CTCAGTGAAG AGGCCTAACT GTCGGGTAAA CTGTAATATG 865
 GCGTAACTGT CGGGTAAACG GCTTTGTCTC CTGACTTCTC CATCTTGAC TTGGCCAGGA 925

AGCCTGGATT GTTCAACCAC TTAGTTCTAA AGAACTGTTT TCTGTTTTG CCGAAGGTTG 985
 TATTGTATGT TTTAGTCAAA AATATTAGTA GGAAAATGGC TTACTAGTAT AACACTGAAG 1045
 TTCATTATGC AATGTTTAA TAAAATATTG TGCTTGAGT TATTAAAGTT TGATATATAC 1105
 TCTTAAAATC ATTAAACTAA TTCATCAATT AAATG 1140

(2) INFORMATION FOR SEQ ID NO: 2:

By Cont
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys Val Leu Ser Ser His
 1 5 10 15

Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

B1
Cont

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:1..754
(D) OTHER INFORMATION:/note= "Human SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC C¹TG GCC TCT CAC
Met Ala Asp Val Glu Asp Gly Glu Thr Cys Ala Leu Ala Ser His
5 10 15

48

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

96

41 → 123

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

144

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

192

237 261

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

240

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

288

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

336

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTAGAG CCCTGGTGGAA
Lys

389

TCTTGTAATC CAGTGCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG

449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT

509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC

569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT

629

GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAAGCAGT TTGAGACTT

689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT

749

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Bl
Cont Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide P1
downstream primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAGCTTTTTT TTTTTTTR

18

(2) INFORMATION FOR SEQ ID NO: 6:

Bl
Cont

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide: P2
upstream primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AAGCTTNNNN NNN

13

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide SAG TA.01"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGGGATCCCC ATGGCCGACG TGAGG

25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAG T.02"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CGGGATCCTC ATTTGCCGAT TCTTTG

26

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

Part

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide P.01"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TATGGCTAGC ATGGCCGACG TGGAGG

26

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..270

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC

48

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC
 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT
 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

ACG TGC GCC ATC TGC AGG GTC CAG ATG CCT GTC TTA GAT GTC AAG CTG
 Thr Cys Ala Ile Cys Arg Val Gln Met Pro Val Leu Asp Val Lys Leu
 50 55 60

AAA ACA AAC AAG AGG ACT GTG TTG TGG TCT GGG GAG AAT GTA ATC ATT
 Lys Thr Asn Lys Arg Thr Val Leu Trp Ser Gly Glu Asn Val Ile Ile
 65 70 75 80

CCT TCC ACA ACT GCT GCA TGT CCC TGT GGG TGAAACAGAA CAATCGCTGC
 Pro Ser Thr Thr Ala Ala Cys Pro Cys Gly
 85 90

CCTCTCTGCC AGCAGGACTG GGTGGTCCAA AGAACATCGCA AATGAGAGTG GTTAGAAGGC
 TTCTTAGCGC AGTTGTTCAAG AGCCCTGGTG GATCTGTAA TCCAGTGCCT TACAAAGGCT
 AGAACACTAC AGGGGATGAA TTCTTCAAAT AGGAGCCGAT GGATCTGTGG TCTTGGACT
 CATCAAAGCC TTGGTTAGCA TTTGTCAGTT TTATCTTCAG AAATTCTCTG TGATTAAGAA
 GATAATTAT TAAAGGTGGT CCTTCCTACC TCTGTGGTGT GTGTCGCGCA CACAGCTTAG
 AAGTGCTATA AAAAAGGAAA GAGCTCCAAA TTGAATCACC TTATAATTAA CCCATTTCTA
 TACAACAGGC AGTGGAAAGCA GTTTCGAGAC TTTTCGATG CTTATGGTTG ATCAGTTAAA
 AAAGAATGTT ACAGTAACAA ATAAAGTGCA GTTTAAA

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

35

40

45

Thr Cys Ala Ile Cys Arg Val Gln Met Pro Val Leu Asp Val Lys Leu
50 55 60

Lys Thr Asn Lys Arg Thr Val Leu Trp Ser Gly Glu Asn Val Ile Ile
65 70 75 80

Pro Ser Thr Thr Ala Ala Cys Pro Cys Gly
85 90

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..291

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:1..291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1			5						10					15		

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96
 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT 144
 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

```

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GTG GTC TGG GGA GAA TGT      192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys
      50          55          60

```

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC 240
 Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 65 70 75 80

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC 288
 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 85 90 95

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA 341
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG 401
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT 461
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTATTA AAGGTGGTCC TTCCTACCTC 521
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 581
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAAGCAGT TTCGAGACTT 641
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT 701
TTAAA 706

Part

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys
50 55 60

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
65 70 75 80

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
85 90 95

Lys

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide hSAG. M1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCCATCTGCA GGGTCCAG

18

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAG T.02L"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGATCCTCAT TTGCCGATTC TTTGGAC

27

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAGKanMX4-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTCTCCAGTG GCAGAGAACT TTAAAGAGAA ATAGTTCAAC CGTACGCTGC AGGTCGAC

58

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAGKan MX
4-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

ACCTCGGTAT GATTAAATG TTTACGGGCA ATTCACTTTT ATCGATGAAT TCGAGCTCG

59

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Bob
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTCTCCAGTG GCAGAGAAC

19

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATGATTAAA TGTTTACGGG C

21

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1		5					10					15				
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	
20		25										30				
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35							40					45				
ACG	AGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	TGT	192
Thr	Ser	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys	
50							55					60				
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Val	Trp	Glu	Cys	
65		70						75					80			
AAT	CAT	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
85								90					95			
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
100								105					110			
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTAGAG	CCCTGGTGG											389
Lys																
TCTTGTAAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG											449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTATTA	AAGGTGGTCC	TTCCCTACCTC											569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629
GAATCACCTT	ATAATTTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT											689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT											749
TTAAA																754

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Ser Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1			5						10						15	
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	
20			25												30	
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35			40												45	
ACG	TGC	GCC	ATC	AGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	TGT	192
Thr	Cys	Ala	Ile	Ser	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys	
50			55												60	
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys	
65		70													80	
AAT	CAT	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
85			90												95	
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
100			105												110	
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTAGAG	CCCTGGTGG											389
Lys																
TCTTGTAAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG											449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTATTA	AAGGTGGTCC	TTCCTACCTC											569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629
GAATCACCTT	ATAATTTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT											689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT											749
TTAAA																754

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15
 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30
 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45
 Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60
 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80
 Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95
 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110
 Lys

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	

35	40	45	
ACG AGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT			192
Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys			
50	55	60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT			240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys			
65	70	75	80
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC			288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn			
85	90	95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC			336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly			
100	105	110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA			389
Lys			
TCTTGTAAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG			449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAAGTTT			509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTATTA AAGGTGGTCC TTCCTACCTC			569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT			629
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT			689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT			749
TTAAA			754

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His			
1	5	10	15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu			
20	25	30	

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp			
35	40	45	

Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys

50	55	60													
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys
65					65	70			75			80			
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn
					85				90			95			
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly
					100			105			110				

Lys

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..339
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATG	GCC	GAC	GTG	GAA	GAC	GGG	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1			5					10						15		
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGG	GAC	AAG	ATG	TTC	TCC	CTC		96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	
						20		25						30		
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
						35		40						45		
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	AGT	CTT	AGA	TGT	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Ser	Leu	Arg	Cys	
						50		55						60		
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys	
					65		70			75			80			
AAT	CAT	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn		
85	90	95
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336	
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly		
100	105	110
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA	389	
Lys		
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449	
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509	
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTATTA AAGGTGGTCC TTCCTACCTC	569	
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629	
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAAGCAGT TTCGAGACTT	689	
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749	
TTAAA	754	

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His			
1	5	10	15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu			
20	25	30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp			
35	40	45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Cys			
50	55	60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys			
65	70	75	80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn			
85	90	95	
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly			
100	105	110	

Lys

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1			5					10						15		
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
20						25								30		
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35						40							45			
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	TGT	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys	
50						55						60				
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	AGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Ser	
65						70				75				80		
AAT	CAT	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
85						90							95			
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
100						105						110				
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTCAAGAG	CCCTGGTGG											389
Lys																

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTACCA CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Ser
 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG	GCC	GAC	GTG	GAA	GAC	GGG	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1			5					10				15				
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGG	GAC	AAG	ATG	TTC	TCC	CTC	96	
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	
20			25					30								
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35				40							45					
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	TGT	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys	
50				55				60								
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys	
65				70				75				80				
AAT	AAA	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	Lys	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
85				90								95				
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
100					105							110				
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTAGAG	CCCTGGTGG											389
Lys																
TCTTGTAAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG											449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTATTA	AAGGTGGTCC	TTCCTACCTC											569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629
GAATCACCTT	ATAATTCTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT											689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT											749

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn Lys Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATG	GCC	GAC	GTG	GAA	GAC	GGG	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1		5							10					15		
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGG	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	
20		25										30				
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35							40					45				
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	TGT	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys	
50							55					60				
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Val	Trp	Glu	Cys	
65		70							75				80			
AAT	CAT	TCC	TTC	AAG	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	Ser	Phe	Lys	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn		
85								90					95			
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
100								105					110			
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTAGAG	CCCTGGTGG											389
Lys																
TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG											449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTATTA	AAGGTGGTCC	TTCCTACCTC											569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629
GAATCACCTT	ATAATTCTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT											689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT											749
TTAAAA																754

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45	144
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60	192
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80	240
AAT CAT TCC TTC CAC AAC TGC AGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Ser Met Ser Leu Trp Val Lys Gln Asn 85 90 95	288
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110	336
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGAA Lys	389
TCTTGTAAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT TTAAA	449 509 569 629 689 749 754

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Ser Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT 144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT 192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT 240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 c 80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC AGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Ser Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAAGTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCAC A CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
Asn Arg Ser Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	

100

105

110

Lys

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

*B1
CDS*

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1			5					10						15		
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
20			25										30			
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35			40									45				
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	TGT	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys	
50			55								60					
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys	
65		70							75				80			
AAT	AAA	TCC	TTC	AAG	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	Lys	Ser	Phe	Lys	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
85			90									95				
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
100			105									110				
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTCAAGAG	CCCTGGTGGA											389
Lys																

TCTTGTAAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAAGTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTACCA CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 . 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80

Asn Lys Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1		5					10					15				
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	
20		25										30				
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35							40					45				
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	AGT	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Ser	
50							55					60				
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys	
65		70						75				80				
AAT	CAT	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
85								90				95				
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
100								105				110				
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTAGAG	CCCTGGTGG											389
Lys																
TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG											449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTATTA	AAGGTGGTCC	TTCCCTACCTC											569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629
GAATCACCTT	ATAATTAC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT											689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Ser
 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..339

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide

(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATG	GCC	GAC	GTG	GAA	GAC	GGG	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1	5								10					15		
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGG	GAC	AAG	ATG	TTC	TCC	CTC	96	
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	
20	25													30		
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35							40					45				
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	TGT	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys	
50							55				60					
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	AGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Ser	Val	Val	Val	Trp	Gly	Glu	Cys	
65							70			75			80			
AAT	CAT	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn		
85							90					95				
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
100							105				110					
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTAGAG	CCCTGGTGG											389
Lys																
TCTTGTAAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG											449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTATTA	AAGGTGGTCC	TTCCCTACCTC											569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629
GAATCACCTT	ATAATTTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT											689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT											749
TTAAA																754

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Ser Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu

	20	25	30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT				144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp				
35	40	45		
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC AGT CTT AGA AGT				192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Ser				
50	55	60		
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT				240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys				
65	70	75	80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC				288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn				
85	90	95		
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC				336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly				
100	105	110		
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGAA				389
Lys				
TCTTGTAAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG				449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT				509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTATTA AAGGTGGTCC TTCCTACCTC				569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT				629
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT				689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT				749
TTAAA				754

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu

20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Ser
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT 144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT 192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT 240

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	65	70	75	80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC					288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	85	90	95		
AAT CGC AGC CCT CTC AGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC					336
Asn Arg Ser Pro Leu Ser Gln Gln Asp Trp Val Val Gln Arg Ile Gly	100	105	110		
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTAGAG CCCTGGTGGA					389
Lys					
TCTTGTAAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG					449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAAGTTT					509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTATTA AAGGTGGTCC TTCCTACCTC					569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT					629
GAATCACCTT ATAATTCTACC CATTCTATA CAACAGGCAG TGGAAAGCAGT TTCGAGACTT					689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT					749
TTAAA					754

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	1	5	10	15	
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	20	25	30		
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	35	40	45		
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	50	55	60		
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	65	70	75	80	
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	85	90	95		

Asn Arg Ser Pro Leu Ser Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48
Met Ala Asp Val Glu Asp Gly Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG AGC GAT 144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp
35 40 45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT 192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT 240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC 288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC 336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTAGAG CCCTGGTGGA 389
 Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG 449
 GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT 509
 ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTATTA AAGGTGGTCC TTCCTACCTC 569
 TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 629
 GAATCACCTT ATAATTACCA CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT 689
 TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT 749
 TTAAA 754

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp
 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

Lys